



SEQUENCE LISTING

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SEP 16 2003  
TECH CENTER 1600/2900

<110> BOYLE, WILLIAM

<120> OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS

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<140> US 09/721,212

<141> 2000-11-21

<150> US 09/052,521

<151> 1998-03-30

<150> US 08/880,855

<151> 1997-06-23

<150> US 08/842,842

<151> 1997-04-16

<160> 54

<170> PatentIn version 3.1

<210> 1

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Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn	
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<213> Mus musculus

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Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
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Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
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Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
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130 135 140

Met Met Gly Gly Ser Thr Leu Asp Val Ala Gln Arg Gly Lys Pro Glu  
145 150

Ile Arg His Tyr Leu Thr Thr Leu Thr Thr Tyr His Arg Arg Tyr Ile

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195 200 205

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210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
225 230 235 240

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245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
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Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
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• 2011

44222 COS

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35 40 45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val  
50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser  
65 70 75 80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn  
85 90 95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
100 105 110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
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165 170 175

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180 185 190

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195 200 205

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210 215 220



Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
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Sequence of the DNA fragment

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Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu Ala Leu Cys Val Leu Leu	
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Val Pro Leu Gln Val Thr Leu Gln Val Thr Pro Pro Cys Thr Gln Glu	
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Arg His Tyr Glu His Leu Gly Arg Cys Cys Ser Arg Cys Glu Pro Gly	
40 45 50	
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Gly	Gly	Pro	Trp	Ala	Gln	Val	Arg	Asp	Ser	Arg	Thr	Phe	Thr	Leu	Val		
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Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	Cys	Phe	Thr	Gly	Thr	Glu		
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Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	Ser	Ser	Asn	Ser	Thr	Asp		
		425					430					435					
ggc tac aca ggc agt ggg aac act cct ggg gag gac cat gaa ccc ttt 1397																	
Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly	Glu	Asp	His	Glu	Pro	Phe		
		440				445					450						
cca ggg tcc ctg aaa tgt gga cca ttg ccc cag tgt gcc tac agc atg 1445																	
Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro	Gln	Cys	Ala	Tyr	Ser	Met		
					460					465					470		
ggc ttt ccc agt gaa gca gca gcc agc atg gca gag gcg gga gta cgg 1493																	
Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met	Ala	Glu	Ala	Gly	Val	Arg		
				475					480					485			
ccc cag gac agg gct gat gag agg gga gcc tca ggg tcc ggg agc tcc 1541																	
Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala	Ser	Gly	Ser	Gly	Ser	Ser		
			490					495					500				
ccc agt gac cag cca cct gcc tct ggg aac gtg act gga aac agt aac 1589																	
Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	Ser	Asn		
		505					510					515					
tcc acg ttc atc tct agc ggg cag gtg atg aac ttc aag ggt gac atc 1637																	
Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	Asp	Ile		
		520				525					530						
atc gtg gtg tat gtc agc cag acc tcc cag gag ggc ccg ggt tcc gca 1685																	
Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Pro	Gly	Ser	Ala		
		535			540				545					550			
gag ccc gag tcc gag ccc gtg ggc cgc cct gtg cag gag gag acc ctg 1733																	
Glu	Pro	Glu	Ser	Glu	Pro	Val	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu		
				555				560					565				
gca cac aga gac tcc ttt gcg ggc acc gcg ccg cgc ttc ccc gac gtc 1781																	
Ala	His	Arg	Asp	Ser	Phe	Ala	Gly	Thr	Ala	Pro	Arg	Phe	Pro	Asp	Val		
			570				575						580				

Leu His Thr Gln Gly Ser Gly Gln Cys Ala Glu  
615 620 625

gacctgggtg cagggcacca gtgcctttcc aaaaacatgg ttagctagc cactgtgcac 1990  
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Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys  
35 40 45

Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr  
50 55 60

Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr  
65 70 75 80

Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Tyr  
85 90 95

Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg  
100 105 110

Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys

115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200

Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys  
165 170 175

Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp  
180 185 190

Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala  
195 200 205

Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val  
210 215 220

Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly  
225 230 235 240

Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser  
245 250 255

Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser  
260 265 270

His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu  
275 280 285

Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys  
290 295 300

Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser  
305 310 315 320

Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser  
325 330 335

Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro  
340 345 350

Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro  
355 360 365

Pro Phe Gln Gln Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln

Pro Leu Thr Thr Ser Asn Ile Arg Ser Met Ile Thr Ser Ile Lys Tyr



His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val  
420 425 430

Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly  
435 440 445

Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro  
450 455 460

Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met  
465 470 475 480

Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala  
485 490 495

Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn  
500 505 510

Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met  
515 520 525

Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln  
530 535 540

Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro  
545 550 555 560

Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala  
565 570 575

Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Gln Gln  
580 585 590

Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Gln Gln  
595 600 605

Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala  
610 615 620

Gln

11111

11111 1111

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Met Lys Gln Ala Phe Gln Gln Asp Ile Asp  
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Met Glu Gly Ser Trp Gln Asp Ile Asp  
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<212> PRT

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1 5

<210> 51

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<400> 52

Met His Leu Thr Ile Gln Asp Ile Asp  
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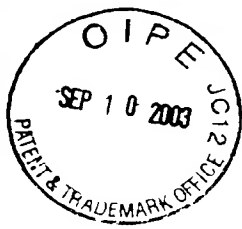
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Met Ile Thr Asp Ala Thr Asp Thr Asp



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Lys Leu Val Thr Leu Gln Val Thr Pro  
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